

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Murgita, Robert A.

(ii) TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A CELL PROLIFERATIVE AGENT

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/377,316
(B) FILING DATE: 24-JAN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
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(C) REFERENCE/DOCKET NUMBER: 06727/006001

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATATTGTGCT TCCACCACTG CCAATAACAA AATAACTAGC AACCATGAAG TGGGTGGAAT	60
CAATTTTTT AATTTCTTA CTAAATTTA CTGAATCCAG AACACTGCAT AGAAATGAAT	120
ATGGAATAGC TTCCATATTG GATTCTTACC AATGTACTGC AGAGATAAGT TTAGCTGACC	180
TGGCTACCAT ATTTTTGCC CAGTTGTTC AAGAAGCCAC TTACAAGGAA GTAAGAAAA	240

TGGTGAAAGA TGCATTGACT GCAATTGAGA AACCCACTGG AGATGAACAG TCTTCAGGGT 300
 GTTTAGAAAA CCAGCTACCT GCCTTCTGG AAGAACTTTG CCATGAGAAA GAAATTTGG 360
 AGAAAGTACGG ACATTCAGAC TGCTGCAGCC AAAGTGAAGA GGGAGACAT AACTGTTTC 420
 TTGCACACAA AAAGCCCAGT GCAGCATGGA TCCCACCTTT CCAAGTTCCA GAACCTGTCA 480
 CAAGCTGTGA AGCATATGAA GAAGACAGGG AGACATTCAAT GAAACAAATTC ATTTATGAGA 540
 TAGCAAGAAG GCATCCCTTC CTGTATGCAC CTACAATTCT TCTTCGGCT GCTGGGTATG 600
 AGAAAATAAT TCCATCTTGC TGCAAAGCTG AAAATGCAGT TGAATGCTTC CAAACAAAGG 660
 CAGCAACAGT TACAAAAGAA TTAAGAGAAA GCAGCTTGT AAATCAACAT GCATGTCCAG 720
 TAATGAAAAA TTTTGGGACC CGAACTTTCC AAGCCATAAC TGTTACTAAA CTGAGTCAGA 780
 AGTTTACCAA AGTTAATTTC ACTGAAATCC AGAAACTAGT CCTGGATGTG GCCCATGTAC 840
 ATGAGCACTG TTGCAGAGCA GATGTGCTGG ATTGTCTGCA GGATGGGAA AAAATCATGT 900
 CCTACATATG TTCTCAACAA GACACTCTGT CAAACAAAAT AACAGAATGC TGCAAACGTGA 960
 CCACGCTGGA ACGTGGTCAA TGTATAATTG ATGCAGAAAA TGATGAAAAA CCTGAAGGTC 1020
 TATCTCCAAA TCTAAACAGG TTTTAGGAG ATAGAGATTT TAACCAATTG TCTTCAGGGG 1080
 AAAAAAAATAT CTTCTGGCA AGTTTGTTC ATGAATATTG AAGAAGACAT CCTCAGCTTG 1140
 CTGTCTCAGT AATTCTAAGA GTTGCTAAAG GATACCAGGA GTTATTGGAG AAGTGTTC 1200
 AGACTGAAAA CCCTCTGAA TGCCAAGATA AAGGAGAAGA AGAATTACAG AAATACATCC 1260
 AGGAGAGCCA AGCATTGGCA AAGCGAAGCT GCGGCCTCTT CCAGAAACTA GGAGAATATT 1320
 ACTTACAAAAA TGAGTTCTC GTTGCTTACA CAAAGAAAGC CCCCCAGCTG ACCTCGTCGG 1380
 AGCTGATGGC CATCACCCAGA AAAATGGCAG CCACAGCAGC CACTTGTGCA CAACTCAGTG 1440
 AGGACAAACT ATTGGCCTGT GGCGAGGGAG CGGCTGACAT TATTATCGGA CACTTATGTA 1500
 TCAGACATGA AATGACTCCA GTAAACCCCTG GTGTTGGCCA GTGCTGCACT TCTTCATATG 1560
 CCAACAGGAG GCCATGCTTC AGCAGCTTG TGTTGGATGA AACATATGTC CCTCCTGCAT 1620
 TCTCTGATGA CAAGTTCATT TTCCATAAGG ATCTGTGCCA AGCTCAGGGT GTAGCGCTGC 1680
 AAAGGATGAA GCAAGAGTTT CTCATTAACC TTGTGAAGCA AAAGCCACAA ATAACAGAGG 1740
 AACAACTTGA GGCTCTCATT GCAGATTCT CAGGCCTGTT GGAGAAATGC TGCCAAGGCC 1800
 AGGAACAGGA AGTCTGCTTT GCTGAAGAGG GACAAAAACT GATTTCAAAA ACTGGTGCTG 1860
 CTTTGGGAGT TTAAATTACT TCAGGGGAAG AGAAGACAAA ACGAGTCTTT CATTGGTGT 1920
 GAACTTTCT CTTTAATTTC AACTGATTG AACTTTTG TGAATTAATG ATAAAGACTT 1980
 TTATGTGAGA TTTCTTATC ACAGAAATAA AATATCTCCA AA 2022

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr
1 5 10 15

Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe
20 25 30

Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val
35 40 45

Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser
50 55 60

Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Leu Cys
65 70 75 80

His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser
85 90 95

Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro
100 105 110

Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser
115 120 125

Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile
130 135 140

Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu
145 150 155 160

Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala
165 170 175

Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys
180 185 190

Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Pro Val Met
195 200 205

Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu
210 215 220

Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val
225 230 235 240

Leu Asp Val Ala His Val His Glu His Cys Cys Arg Ala Asp Val Leu
245 250 255

Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln
260 265 270

Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr
275 280 285

Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro
290 295 300

Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe
305 310 315 320

Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val
325 330 335

His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile Leu
340 345 350

Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr
355 360 365

Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys
370 375 380

Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe
385 390 395 400

Gln Lys Leu Gly Glu Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr
405 410 415

Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr
420 425 430

Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp
435 440 445

Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His
450 455 460

Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln
465 470 475 480

Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu
485 490 495

Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe
500 505 510

Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg
515 520 525

Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile
530 535 540

Thr Glu Glu Gln Leu Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu
545 550 555 560

Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu
565 570 575

Gly Gln Lys Leu Ile Ser Lys Thr Gly Ala Ala Leu Gly Val
580 585 590

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr
1 5 10 15

Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe
20 25 30

Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val
35 40 45

Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser
50 55 60

Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu Cys
65 70 75 80

His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser
85 90 95

Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro
100 105 110

Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser
115 120 125

Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile
130 135 140

Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu
145 150 155 160

Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala
165 170 175

Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys
180 185 190

Glu Leu Arg Glu Ser
195

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Leu Leu Asn Gln His Ala Cys Pro Val Met Lys Asn Phe Gly Thr
1 5 10 15

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Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu Ser Gln Lys Phe Thr
20 25 30

Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val Leu Asp Val Ala His
35 40 45

Val His Glu His Cys Cys Arg Ala Asp Val Leu Asp Cys Leu Gln Asp
50 55 60

Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln Gln Asp Thr Leu Ser
65 70 75 80

Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr Leu Glu Arg Gly Gln
85 90 95

Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro Glu Gly Leu Ser Pro
100 105 110

Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe Asn Gln Phe Ser Ser
115 120 125

Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val His Glu Tyr Ser Arg
130 135 140

Arg His Pro Gln Leu Ala Val Ser Val Ile Leu Arg Val Ala Lys Gly
145 150 155 160

Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu
165 170 175

Cys Gln Asp Lys Gly Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser
180 185 190

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu
1 5 10 15

Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro
20 25 30

Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala
35 40 45

Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys
50 55 60

Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His
65 70 75 80

Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser
85 90 95
Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr
100 105 110
Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp
115 120 125
Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg Met Lys Gln Glu Phe
130 135 140
Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu
145 150 155 160
Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln
165 170 175
Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile
180 185 190
Ser Lys Thr Gly Ala Ala Leu Gly Val
195 200

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr
1 5 10 15
Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe
20 25 30
Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val
35 40 45
Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser
50 55 60
Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu Cys
65 70 75 80
His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser
85 90 95
Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro
100 105 110
Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser
115 120 125
Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile

130 135 140

Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu
145 150 155 160

Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala
165 170 175

Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys
180 185 190

Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Pro Val Met
195 200 205

Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu
210 215 220

Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val
225 230 235 240

Leu Asp Val Ala His Val His Glu His Cys Cys Arg Ala Asp Val Leu
245 250 255

Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln
260 265 270

Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr
275 280 285

Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro
290 295 300

Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe
305 310 315 320

Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val
325 330 335

His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile Leu
340 345 350

Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr
355 360 365

Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys
370 375 380

Tyr Ile Gln Glu Ser
385

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Leu Leu Asn Gln His Ala Cys Pro Val Met Lys Asn Phe Gly Thr
1 5 10 15

Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu Ser Gln Lys Phe Thr
20 25 30

Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val Leu Asp Val Ala His
35 40 45

Val His Glu His Cys Cys Arg Ala Asp Val Leu Asp Cys Leu Gln Asp
50 55 60

Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln Gln Asp Thr Leu Ser
65 70 75 80

Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr Leu Glu Arg Gly Gln
85 90 95

Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro Glu Gly Leu Ser Pro
100 105 110

Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe Asn Gln Phe Ser Ser
115 120 125

Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val His Glu Tyr Ser Arg
130 135 140

Arg His Pro Gln Leu Ala Val Ser Val Ile Leu Arg Val Ala Lys Gly
145 150 155 160

Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu
165 170 175

Cys Gln Asp Lys Gly Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser
180 185 190

Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu
195 200 205

Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro
210 215 220

Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala
225 230 235 240

Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Ala Cys
245 250 255

Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His
260 265 270

Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser
275 280 285

Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr
290 295 300

Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp
305 310 315 320

Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg Met Lys Gln Glu Phe
325 330 335

Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu

340

345

350

Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln
355 360 365

Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile
370 375 380

Ser Lys Thr Gly Ala Ala Leu Gly Val
385 390

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Handwritten mark: A/
Met Ser Tyr Ile Cys Ser Gln Gln Asp Thr Leu Ser Asn Lys Ile Thr
1 5 10 15

Glu Cys Cys Lys Leu Thr Thr Leu Glu Arg Gly Gln Cys Ile Ile His
20 25 30

Ala Glu Asn Asp Glu Lys Pro Glu Gly Leu Ser Pro Asn Leu Asn Arg
35 40 45

Phe Leu Gly Asp Arg Asp Phe Asn Gln Phe Ser Ser Gly Glu Lys Asn
50 55 60

Ile Phe Leu Ala Ser Phe Val His Glu Tyr Ser Arg Arg His Pro Gln
65 70 75 80

Leu Ala Val Ser Val Ile Leu Arg Val Ala Lys Gly Tyr Gln Glu Leu
85 90 95

Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu Cys Gln Asp Lys
100 105 110

Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser Gln Ala Leu Ala
115 120 125

Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu Tyr Tyr Leu Gln
130 135 140

Asn Glu Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro Gln Leu Thr Ser
145 150 155 160

Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala Thr Ala Ala Thr
165 170 175

Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala
180 185 190

Ala Asp Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro
195 200 205

33

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg
210 215 220
Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro
225 230 235 240
Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala
245 250 255
Gln Gly Val Ala Leu Gln Arg Met Lys Gln Glu Phe Leu Ile Asn Leu
260 265 270
Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Leu Ile
275 280 285
Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln
290 295 300
Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Gly
305 310 315 320
Ala Ala Leu Gly Val
325

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Can* (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAAGGTA CCACACTGCA TAGAAATGAA 30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAAAAAGGAT CCTTAGCTTT CTCTTAATTC TTT 33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAAAAAATCG ATATGAGCTT GTTAAATCAA CAT

33

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAAAAAAGGAT CCTTAGCTCT CCTGGATGTA TTT

33

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAAAAATCG ATATGCAAGC ATTGGCAAAG CGA

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAAAAAAGGAT CCTTAAACTC CCAAAGCAGC ACG

33

(2) INFORMATION FOR SEQ ID NO:15:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAAAAAATCG ATATGTCCTA CATATGTTCT CAA

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Tyr Ile Cys Ser Gln Gln Asp Thr
1 5
